



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Oon, Chong Jin
Lim, Gek Keow
Leong, Ai Lin
Zhao, Yi
Chen, Wei Ning
- (ii) TITLE OF INVENTION: A VACCINE-INDUCED HEPATITIS B VIRAL STRAIN AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Ladas & Parry
 - (B) STREET: 26 West 61 Street
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10023
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/719,533
 - (B) FILING DATE: 13-DEC-2000
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/SG98/00045
 - (B) FILING DATE: 19-JUN-1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Mass, Clifford J.
 - (B) REGISTRATION NUMBER: 30,086
 - (C) REFERENCE/DOCKET NUMBER: U-013108-9
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 708-1890

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| CTCCACCACT TTCCACCAAA CTCTTCAAGA TCCCAGAGTC AGGGCCCTGT ACTTTCCTGC | 60 |
| TGGTGGCTCC AGTTCAGGAA CAGTGAGCCC TGCTCAGAAT ACTGTCTCTG CCATATCGTC | 120 |
| AATCTTATCG AAGACTGGGG ACCCTGTACC GAACATGGAG AACATCGCAT CAGGACTCCT | 180 |
| AGGACCCCTG CTCGTGTTAC AGGCGGGGTT TTTCTTGTTG ACAAAAATCC TCACAATACC | 240 |
| GCAGAGTCTA GACTCGTGGT GGACTTCTCT CAATTTTCTA GGGGGAACAC CCGTGTGTCT | 300 |

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|-------------|------------|------------|------------|-------------|-------------|------|
| TGGCCAAAAT | TCGCAGTCCC | AAATCTCCAG | TCACTCACCA | ACCTGTTGTC | CTCCAATTTG | 360 |
| TCCTGGTTAT | CGCTGGATGT | GTCTGCGGCG | TTTTATCATC | TTCCTCTGCA | TCCTGCTGCT | 420 |
| ATGCCTCATC | TTCTTGTTGG | TTCTTCTGGA | CTATCAAGGT | ATGTTGCCCCG | TTTGTCTCTT | 480 |
| AATTCCAGGA | TCAACAACAA | CCAGCACCGG | ACCATGCAAA | ACCTGCACAA | CTCCTGCTCA | 540 |
| AGGAACCTCT | ATGTTTCCCT | CATGTTGCTG | TACAAAACCT | ACGGACAGAA | ACTGCACCTG | 600 |
| TATTCCCATC | CCATCATCTT | GGGCTTTTCG | AAAATACCTA | TGGGAGTGGG | CCTCAGTCCG | 660 |
| TTTCTCTTGG | CTCAGTTTAC | TAGTGCCATT | TGTTCACTGG | TTCGTAGGGC | TTTCCCCCAC | 720 |
| TGTCTGGCTT | TCAGTTATAT | GGATGATGTG | GTTTTGGGGG | CCAAGTCTGT | ACAACATCTT | 780 |
| GAGTCCCTTT | ATGCCGCTGT | TACCAATTTT | CTTTTGTCTT | TGGGTATACA | TTTAAACCTT | 840 |
| CACAAAACAA | AAAGATGGGG | ATATTCCCTT | AACTTCATGG | GATATGTCAT | TGGGAGTTGG | 900 |
| GGCACATTGC | CACAGGAACA | TATTGTACAA | AAAATCAAAA | TGTGTTTTAG | GAAACTTCCT | 960 |
| GTAAACAGGC | CTATTGATTG | GAAAGTATGT | CAACGAATTG | TGGGTCTTTT | GGGGTTTGCC | 1020 |
| GCCCCTTTCA | CGCAATGTGG | ATATCCTGCT | TTAATGCCTT | TATATGCATG | TATACAAGCA | 1080 |
| AAACAGGCTT | TTACTTTCTC | GCAAACCTAC | AAGACCTTTC | TAAGTAAACA | GTATCTGAAC | 1140 |
| CTTTACCCCG | TTGCTCGGCA | ACGCCCTGGT | CTGTGCCAAG | TGTTTGCTGA | CGCAACCCCC | 1200 |
| ACTGGTTGGG | GCTTGGCCAT | AGGCCATCAG | CGCATGCGTG | GAACCTTTGT | GTCTCCTCTG | 1260 |
| CCGATCCATA | CTGCGGAACT | CCTAGCCGCT | TGTTTTGCTC | GCAGCAGGTC | TGGGGCAAAA | 1320 |
| CTCATCGGGA | CTGACAATTC | TGTCGTGCTC | TCCCGCAAGT | ATACATCATT | TCCATGGCTG | 1380 |
| CTAGGCTGTG | CTGCCAACTG | GATCCTGCGC | GGGACGTCCT | TTGTTTACGT | CCCGTCGGCG | 1440 |
| CTGAATCCCG | CGGACGACCC | CTCCCGGGGC | CGCTTGGGGC | TCTACCGCCC | GCTTCTCCGC | 1500 |
| CTGTTATACC | GACCGACCAC | GGGGCGCACC | TCTCTTTACG | CGGACTCCCC | GTCTGTGCCT | 1560 |
| TCTCATCTGC | CGGACCGTGT | GCACTTCGCT | TCACCTCTGC | ACGTCGCATG | GAGACCACCG | 1620 |
| TGAACGCCCC | CGGGAACCTG | CCCAAGGTCT | TGCATAAGAG | GACTCTTGGA | CTTTCAGCAA | 1680 |
| TGTCAACGAC | CGACCTTGAG | GCATACTTCA | AAGACTGTGT | GTTTAATGAG | TGGGAGGAGT | 1740 |
| TGGGGGAGGA | GGTTAGGTTA | AAGGTCTTTG | TACTAGGAGG | CTGTAGGCAT | AAATTGGTGT | 1800 |
| GTTCAACCATC | ACCATGCAAC | TTTTTCACCT | CTGCCTAATC | ATCTCATGTT | CATGTCCTAC | 1860 |
| TGTTCAAGCC | TCCAAGCTGT | GCCTTGGGTG | GCTTTGGGGC | ATGGACATTG | ACCCGTATAA | 1920 |
| AGAAATTGGA | GCTTCTGTGG | AGTTACTCTC | TTTTTTGCCT | TCTGACTTTT | TTCTTCTAT | 1980 |
| TCGAGATCTC | CTCGACACCG | CCTCTGCTCT | GTATCGGGAG | GCCTTAGAGT | CTCCGGAACA | 2040 |
| TTGTTACACT | CACCATACGG | CACTCAGGCA | AGCTATTCTG | AGTTGGGGTG | AGTTAATGAA | 2100 |
| TCTAGCCACC | TGGGTGGGAA | GTAATTTGGA | AGATCCAGCA | TCCAGGGAAT | TAGTAGTCAG | 2160 |
| CTATGTCAAC | GTTAATATGG | GCCTAAAAAT | CAGACAACTA | TTGTGGTTTC | ACATTTCCCTG | 2220 |
| TCTTACTTTT | GGGAGAGAAA | CTGTTCTTGA | ATATTTGGTG | TCTTTTGGAG | TGTGGATTCTG | 2280 |

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|--|------|
| CACTCCTCCT GCATATAGAC CACCAAATGC CCCTATCTTA TCAACACTTC CGGAAACTAC | 2340 |
| TGTTGTTAGA CGAAGAGGCA GGTCCCCTAG AAGAAGAACT CCCTCGCCTC GCAGACGAAG | 2400 |
| GTCTCAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGGAA TCTCAATGTT AGTATTCCTT | 2460 |
| GGACACATAA GGTGGGAAAC TTTACGGGGC TTTATTCTTC TACGGTACCT TGCTTTAATC | 2520 |
| CTAAATGGCA AACTCCTTCT TTTCCGGACA TTCATTGCA GGAGGACATT CTTGATAGAT | 2580 |
| GTAAGCAATT TGTGGGGCCC CTTACAGTAA ATGAAAACAG GAGACTAAAA TTAATTATGC | 2640 |
| CTGCTAGGTT TTATCCAAAT GTTACTAAAT ATTTGCCCTT AGATAAAGGG ATCAAACCAT | 2700 |
| ATTATCCAGA GTATGTAGTT AATCATTACT TCCAGACGCG ACATTATTTA CAACTCTTT | 2760 |
| GGAAGGCGGG GATCTTATAT AAAAGAGAGT CCACACGTAG CGCCTCATTT TGCGGGTCAC | 2820 |
| CATATTCTTG GGAACAAGAT CTACAGCATG GGAGGTTGGT CTTCCAAACC TCGAAAAGGC | 2880 |
| ATGGGGACAA ATCTTTCTGT CCCCAATCCC CTGGGATTCT TCCCCGATCA TCAGTTGGAC | 2940 |
| CCTGCATTCA AAGCCAACCTC AGAAAATCCA GATTGGGACC TCAACCCGCA CAAGGACAAC | 3000 |
| TGGCCGGACG CCAACAAGGT GGGAGTGGGA GCATTGCGGC CAGGGTTCAC CCCTCCTCAT | 3060 |
| GGGGGACTGT TGGGGTGGAG CCCTCAGGCT CAGGGCCTAC TCACAACTGT GCCAGCAGCT | 3120 |
| CCTCCTCCTG CCTCCACCAA TCGGCAGTCA GGAAGGCAGC CTACTCCCTT ATCTCCACCT | 3180 |
| CTAAGGGACA CTCATCCTCA GGCCATGCAG TGGAA | 3215 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Leu | Ser | Tyr | Gln | His | Phe | Arg | Lys | Leu | Leu | Leu | Leu | Asp | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Ala | Gly | Pro | Leu | Glu | Glu | Glu | Leu | Pro | Arg | Leu | Ala | Asp | Glu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Asn | Arg | Arg | Val | Ala | Glu | Asp | Leu | Asn | Leu | Gly | Asn | Leu | Asn | Val |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ser | Ile | Pro | Trp | Thr | His | Lys | Val | Gly | Asn | Phe | Thr | Gly | Leu | Tyr | Ser |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Ser | Thr | Val | Pro | Cys | Phe | Asn | Pro | Lys | Trp | Gln | Thr | Pro | Ser | Phe | Pro |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Asp | Ile | His | Leu | Gln | Glu | Asp | Ile | Leu | Asp | Arg | Cys | Lys | Gln | Phe | Val |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Glu | Pro | Leu | Thr | Val | Asn | Glu | Asn | Arg | Arg | Leu | Lys | Leu | Ile | Met | Pro |
| | | | 100 | | | | | 105 | | | | | 110 | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Phe | Tyr | Pro | Asn | Val | Thr | Lys | Tyr | Leu | Pro | Leu | Asp | Lys | Gly | 115 | 120 | 125 |
| Ile | Lys | Pro | Tyr | Tyr | Pro | Glu | Tyr | Val | Val | Asn | His | Tyr | Phe | Gln | Thr | 130 | 135 | 140 |
| Arg | His | Tyr | Leu | His | Thr | Leu | Trp | Lys | Ala | Gly | Ile | Leu | Tyr | Lys | Arg | 145 | 150 | 155 |
| Glu | Ser | Thr | Arg | Ser | Ala | Ser | Phe | Cys | Gly | Ser | Pro | Tyr | Ser | Trp | Glu | 165 | 170 | 175 |
| Gln | Asp | Leu | Gln | His | Gly | Arg | Leu | Val | Phe | Gln | Thr | Ser | Lys | Arg | His | 180 | 185 | 190 |
| Gly | Asp | Lys | Ser | Phe | Cys | Pro | Glu | Ser | Pro | Gly | Ile | Leu | Pro | Arg | Ser | 195 | 200 | 205 |
| Ser | Val | Gly | Pro | Cys | Ile | Gln | Ser | Gln | Leu | Arg | Lys | Ser | Arg | Leu | Gly | 210 | 215 | 220 |
| Pro | Gln | Pro | Ala | Gln | Gly | Gln | Leu | Ala | Gly | Arg | Gln | Gln | Gly | Gly | Ser | 225 | 230 | 235 |
| Gly | Ser | Ile | Arg | Ala | Arg | Val | His | Pro | Ser | Ser | Trp | Gly | Thr | Val | Gly | 245 | 250 | 255 |
| Val | Glu | Pro | Ser | Gly | Ser | Gly | Pro | Thr | His | Asn | Cys | Ala | Ser | Ser | Ser | 260 | 265 | 270 |
| Ser | Ser | Cys | Leu | His | Gln | Ser | Ala | Val | Arg | Lys | Ala | Ala | Tyr | Ser | Leu | 275 | 280 | 285 |
| Ile | Ser | Thr | Ser | Lys | Gly | His | Ser | Ser | Ser | Gly | His | Ala | Val | Glu | Leu | 290 | 295 | 300 |
| His | His | Phe | Pro | Pro | Asn | Ser | Ser | Arg | Ser | Gln | Ser | Gln | Gly | Pro | Val | 305 | 310 | 315 |
| Leu | Ser | Cys | Trp | Trp | Leu | Gln | Phe | Arg | Asn | Ser | Glu | Pro | Cys | Ser | Glu | 325 | 330 | 335 |
| Tyr | Cys | Leu | Cys | His | Ile | Val | Asn | Leu | Ile | Glu | Asp | Trp | Gly | Pro | Cys | 340 | 345 | 350 |
| Thr | Glu | His | Gly | Glu | His | Arg | Ile | Arg | Thr | Pro | Arg | Thr | Pro | Ala | Arg | 355 | 360 | 365 |
| Val | Thr | Gly | Gly | Val | Phe | Leu | Val | Asp | Lys | Asn | Pro | His | Asn | Thr | Ala | 370 | 375 | 380 |
| Glu | Ser | Arg | Leu | Val | Val | Asp | Phe | Ser | Gln | Phe | Ser | Arg | Gly | Asn | Thr | 385 | 390 | 395 |
| Arg | Val | Ser | Trp | Pro | Lys | Phe | Ala | Val | Pro | Asn | Leu | Gln | Ser | Leu | Thr | 405 | 410 | 415 |
| Asn | Leu | Leu | Ser | Ser | Asn | Leu | Ser | Trp | Leu | Ser | Leu | Asp | Val | Ser | Ala | 420 | 425 | 430 |
| Ala | Phe | Tyr | His | Leu | Pro | Leu | His | Pro | Ala | Ala | Met | Pro | His | Leu | Leu | 435 | 440 | 445 |
| Val | Gly | Ser | Ser | Gly | Leu | Ser | Arg | Tyr | Val | Ala | Arg | Leu | Ser | Ser | Asn | 450 | 455 | 460 |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Arg | Ile | Asn | Asn | Asn | Glu | His | Arg | Thr | Met | Glu | Asn | Leu | His | Asn | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Ser | Cys | Ser | Arg | Asn | Leu | Tyr | Val | Ser | Leu | Met | Leu | Leu | Tyr | Lys | Thr | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| Tyr | Gly | Gln | Lys | Leu | His | Leu | Tyr | Ser | His | Pro | Ile | Ile | Leu | Gly | Phe | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |
| Arg | Lys | Ile | Pro | Met | Gly | Val | Gly | Leu | Ser | Pro | Phe | Leu | Leu | Ala | Gln | |
| | | 515 | | | | | 520 | | | | | 525 | | | | |
| Phe | Thr | Ser | Ala | Ile | Cys | Ser | Val | Val | Arg | Arg | Ala | Phe | Pro | His | Cys | |
| | 530 | | | | | 535 | | | | | 540 | | | | | |
| Leu | Ala | Phe | Ser | Tyr | Met | Asp | Asp | Val | Val | Leu | Gly | Ala | Lys | Ser | Val | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| Gln | His | Leu | Glu | Ser | Leu | Tyr | Ala | Ala | Val | Thr | Asn | Phe | Leu | Leu | Ser | |
| | | | | 565 | | | | | 570 | | | | | | 575 | |
| Leu | Gly | Ile | His | Leu | Asn | Pro | His | Lys | Thr | Lys | Arg | Trp | Gly | Tyr | Ser | |
| | | | 580 | | | | | 585 | | | | | 590 | | | |
| Leu | Asn | Phe | Met | Gly | Tyr | Val | Ile | Gly | Ser | Trp | Gly | Thr | Leu | Pro | Gln | |
| | | 595 | | | | | 600 | | | | | 605 | | | | |
| Glu | His | Ile | Val | Gln | Lys | Ile | Lys | Met | Cys | Phe | Arg | Lys | Leu | Pro | Val | |
| | 610 | | | | | 615 | | | | | 620 | | | | | |
| Asn | Arg | Pro | Ile | Asp | Trp | Lys | Val | Cys | Gln | Arg | Ile | Val | Gly | Leu | Leu | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | |
| Gly | Phe | Ala | Ala | Pro | Phe | Thr | Gln | Cys | Gly | Tyr | Pro | Ala | Leu | Met | Pro | |
| | | | | 645 | | | | | 650 | | | | | 655 | | |
| Leu | Tyr | Ala | Cys | Ile | Gln | Ala | Lys | Gln | Ala | Phe | Thr | Phe | Ser | Gln | Thr | |
| | | | 660 | | | | | 665 | | | | | 670 | | | |
| Tyr | Lys | Thr | Phe | Leu | Ser | Lys | Gln | Tyr | Leu | Asn | Leu | Tyr | Pro | Val | Ala | |
| | | 675 | | | | | 680 | | | | | 685 | | | | |
| Arg | Gln | Arg | Pro | Gly | Leu | Cys | Glu | Val | Phe | Ala | Asp | Ala | Thr | Pro | Thr | |
| | 690 | | | | | 695 | | | | | 700 | | | | | |
| Gly | Trp | Gly | Leu | Ala | Ile | Gly | His | Gln | Arg | Met | Arg | Gly | Thr | Phe | Val | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | |
| Ser | Pro | Leu | Pro | Ile | His | Thr | Ala | Glu | Leu | Leu | Ala | Ala | Cys | Phe | Ala | |
| | | | | 725 | | | | | 730 | | | | | 735 | | |
| Arg | Ser | Arg | Ser | Gly | Ala | Lys | Leu | Ile | Gly | Thr | Asp | Asn | Ser | Val | Val | |
| | | | 740 | | | | | 745 | | | | | 750 | | | |
| Leu | Ser | Arg | Lys | Tyr | Thr | Ser | Phe | Pro | Trp | Leu | Leu | Gly | Cys | Ala | Ala | |
| | | 755 | | | | | 760 | | | | | 765 | | | | |
| Asn | Trp | Ile | Leu | Arg | Gly | Thr | Ser | Phe | Val | Tyr | Val | Pro | Ser | Ala | Leu | |
| | 770 | | | | | 775 | | | | | 780 | | | | | |
| Asn | Pro | Ala | Asp | Asp | Pro | Ser | Arg | Gly | Arg | Leu | Gly | Leu | Tyr | Arg | Pro | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | |
| Leu | Leu | Arg | Leu | Leu | Tyr | Arg | Pro | Thr | Thr | Gly | Arg | Thr | Ser | Leu | Tyr | |

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|---|-----|--|-----|--|-----|
| | 805 | | 810 | | 815 |
| Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe | | | | | |
| | 820 | | 825 | | 830 |
| Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro | | | | | |
| | 835 | | 840 | | |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | |
|---|-----|--|-----|--|-----|
| Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu | | | | | |
| 1 | 5 | | 10 | | 15 |
| Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro | | | | | |
| | 20 | | 25 | | 30 |
| Ala Phe Lys Ala Asn Ser Glu Asn Pro Asp Trp Asp Leu Asn Pro His | | | | | |
| | 35 | | 40 | | 45 |
| Lys Asp Asn Trp Pro Asp Ala Asn Lys Val Gly Val Gly Ala Phe Gly | | | | | |
| | 50 | | 55 | | 60 |
| Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln | | | | | |
| | 65 | | 70 | | 75 |
| Ala Gln Gly Leu Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser | | | | | |
| | 85 | | 90 | | 95 |
| Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu | | | | | |
| | 100 | | 105 | | 110 |
| Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His | | | | | |
| | 115 | | 120 | | 125 |
| Gln Thr Leu Gln Asp Pro Arg Val Arg Ala Leu Tyr Phe Pro Ala Gly | | | | | |
| | 130 | | 135 | | 140 |
| Gly Ser Ser Ser Gly Thr Val Ser Pro Ala Gln Asn Thr Val Ser Ala | | | | | |
| | 145 | | 150 | | 155 |
| Ile Ser Ser Ile Leu Ser Lys Thr Gly Asp Pro Val Pro Asn Met Glu | | | | | |
| | 165 | | 170 | | 175 |
| Asn Ile Ala Ser Gly Leu Leu Gly Pro Leu Leu Val Leu Gln Ala Gly | | | | | |
| | 180 | | 185 | | 190 |
| Phe Phe Leu Leu Thr Lys Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser | | | | | |
| | 195 | | 200 | | 205 |
| Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Pro Val Cys Leu Gly | | | | | |
| | 210 | | 215 | | 220 |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asn | Ser | Gln | Ser | Gln | Ile | Ser | Ser | His | Ser | Pro | Thr | Cys | Cys | Pro | 225 | 230 | 235 | 240 |
| Pro | Ile | Cys | Pro | Gly | Tyr | Arg | Trp | Met | Cys | Leu | Arg | Arg | Phe | Ile | Ile | 245 | 250 | 255 | |
| Phe | Leu | Cys | Ile | Leu | Leu | Leu | Cys | Leu | Ile | Phe | Leu | Leu | Val | Leu | Leu | 260 | 265 | 270 | |
| Asp | Tyr | Gln | Gly | Met | Leu | Pro | Val | Cys | Pro | Leu | Ile | Pro | Gly | Ser | Thr | 275 | 280 | 285 | |
| Thr | Thr | Ser | Thr | Gly | Pro | Cys | Lys | Thr | Cys | Thr | Thr | Pro | Ala | Gln | Gly | 290 | 295 | 300 | |
| Thr | Ser | Met | Phe | Pro | Ser | Cys | Cys | Cys | Thr | Lys | Pro | Thr | Asp | Arg | Asn | 305 | 310 | 315 | 320 |
| Cys | Thr | Cys | Ile | Pro | Ile | Pro | Ser | Ser | Trp | Ala | Phe | Ala | Lys | Tyr | Leu | 325 | 330 | 335 | |
| Trp | Glu | Trp | Ala | Ser | Val | Arg | Phe | Ser | Trp | Leu | Ser | Leu | Leu | Val | Pro | 340 | 345 | 350 | |
| Phe | Val | Gln | Trp | Phe | Val | Gly | Leu | Ser | Pro | Thr | Val | Trp | Leu | Ser | Val | 355 | 360 | 365 | |
| Ile | Trp | Met | Met | Trp | Phe | Trp | Gly | Pro | Ser | Leu | Tyr | Asn | Ile | Leu | Ser | 370 | 375 | 380 | |
| Pro | Phe | Met | Pro | Leu | Leu | Pro | Ile | Phe | Phe | Cys | Leu | Trp | Val | Tyr | Ile | 385 | 390 | 395 | 400 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Gln | Leu | Phe | His | Leu | Cys | Leu | Ile | Ile | Ser | Cys | Ser | Cys | Pro | Thr | 1 | 5 | 10 | 15 |
| Val | Gln | Ala | Ser | Lys | Leu | Cys | Leu | Gly | Trp | Leu | Trp | Gly | Met | Asp | Ile | 20 | 25 | 30 | |
| Asp | Pro | Tyr | Lys | Glu | Phe | Gly | Ala | Ser | Val | Glu | Leu | Leu | Ser | Phe | Leu | 35 | 40 | 45 | |
| Pro | Ser | Asp | Phe | Phe | Pro | Ser | Ile | Arg | Asp | Leu | Leu | Asp | Thr | Ala | Ser | 50 | 55 | 60 | |
| Ala | Leu | Tyr | Arg | Glu | Ala | Leu | Glu | Ser | Pro | Glu | His | Cys | Ser | Pro | His | 65 | 70 | 75 | 80 |
| His | Thr | Ala | Leu | Arg | Gln | Ala | Ile | Leu | Ser | Trp | Gly | Glu | Leu | Met | Asn | 85 | 90 | 95 | |
| Leu | Ala | Thr | Trp | Val | Gly | Ser | Asn | Leu | Glu | Asp | Pro | Ala | Ser | Arg | Glu | | | | |

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|---|-----|-----|-----|--|-----|-----|
| | 100 | | 105 | | 110 | |
| Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys Ile Arg Gln | 115 | 120 | 125 | | | |
| Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val | 130 | 135 | 140 | | | |
| Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala | 145 | 150 | 155 | | | 160 |
| Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr | 165 | 170 | 175 | | | |
| Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro | 180 | 185 | 190 | | | |
| Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg | 195 | 200 | 205 | | | |
| Glu Ser Gln Cys | 210 | | | | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | |
|---|-----|-----|-----|----|
| Met Ala Ala Arg Leu Cys Cys Gln Leu Asp Pro Ala Arg Asp Val Leu | 1 | 5 | 10 | 15 |
| Cys Leu Arg Pro Val Gly Ala Glu Ser Arg Gly Arg Pro Leu Pro Gly | 20 | 25 | 30 | |
| Pro Leu Gly Ala Leu Pro Pro Ala Ser Pro Pro Val Ile Pro Thr Asp | 35 | 40 | 45 | |
| His Gly Ala His Leu Ser Leu Arg Gly Leu Pro Val Cys Ala Phe Ser | 50 | 55 | 60 | |
| Ser Ala Gly Pro Cys Ala Leu Arg Phe Thr Ser Ala Arg Arg Met Glu | 65 | 70 | 75 | 80 |
| Thr Thr Val Asn Ala His Gly Asn Leu Pro Lys Val Leu His Lys Arg | 85 | 90 | 95 | |
| Thr Leu Gly Leu Ser Ala Met Ser Thr Thr Asp Leu Glu Ala Tyr Phe | 100 | 105 | 110 | |
| Lys Asp Cys Val Phe Asn Glu Trp Glu Glu Leu Gly Glu Glu Val Arg | 115 | 120 | 125 | |
| Leu Lys Val Phe Val Leu Gly Gly Cys Arg His Lys Leu Val Cys Ser | 130 | 135 | 140 | |
| Pro Ser Pro Cys Asn Phe Phe Thr Ser Ala | 145 | 150 | | |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAAGCTTATG CCCCTATCTT ATCAACACTT CCGGA

35

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTCTAGAC TCTGCGGTAT TGTGA

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCTAGAC TCGTGGTGGA CTTCT

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAATTCT CACGGTGGTC TCCATGCGAC GT

32

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGTTTACG TCCCGT

16

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAAGCTTAG TTTCCGGAAG TGTTGAT